New datapoint 0 New datapoint (1) which category Category 1/2 Category 2 + Category 1 New datapoint assigned to Category STEPS TO FOLLOW IN KNH Step 1 - Choose the number & of neighbours Step 2 - Take the K nearest neighbour of new datapoint, according to the Euclidean distance. Step 3 - Among the K neighbours, count the number of data point in each category where you counted the most neighbours. Your Model is Ready. P₂(x₂,y₂) P₁ and P₂ = Euclidean Distance - $\sqrt{(x_2-x_1)^2+(y_2-y_1)^2}$ TA(KIN) of 2 categories. Category 1 = 3 + 50, based on 3+, new data point is assigned to 't' category. Example -> We need to define the cell types -> stem cells, Blood Vessel Cells, Fat cells Step 1 - Stort with the dataset with know categories. In this case, we have different cell types from a tumos . Then cluster the data in PCAI this case, we used PCA. Step 2 -> Add a new cell, with unknown category to the PCA plot. We don't know this cell category because it was taken from another tumber. So we need to classify the new unknown cell. Step 3 -> We classify the new cell by looking at the nearest annotated Cels (i.e. nearest If is equal to 1, then we only use the nearest neighbour to define the category If K is equal to 11, we would use 11 nearest neighbour and based on majority Based on the most votes, assign the new data point to the class having most votes. NOTE -> If K is odd, then we can avoid ties (equal count to each group) and if we to be severe still get a fied vote, we can thip a coin/decide not to assist

A FEW THOUGHTS ON PICKING A VALUE OF "K".

There is no physical way to determine the best value for "K", so we may have to try out a few values before settling on one.

Tow values for K (like K=1 or K=2) can be noisy and subject to the effects of outliers.

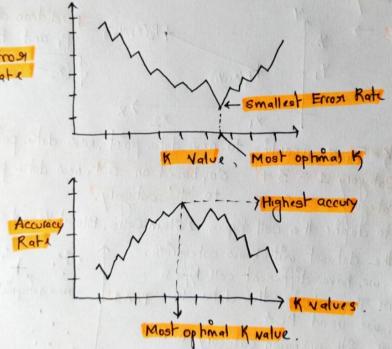
that a category with only a few samples in it will always be pod voted by other categories.

In general practise, choosing the value of K is K = sgrt (N) where M stands

for Number of samples in training dataset.

Another way to choose K is through cross-validation. One way to select different possible value of K and cheek for what value of K gives us the best performance on validation set

-> use an error plot or accuracy plot to find the most favourable is value.



and high variance. The variance is due to the fact that the prediction in a given region is entirely dependent on just one observation.

tegion is an average of sexa, several points and so changing one observation has smaller effects. However smoothing may cause bias. High bias, low variance.